RAW SEQUENCE LISTING ERROR REPORT
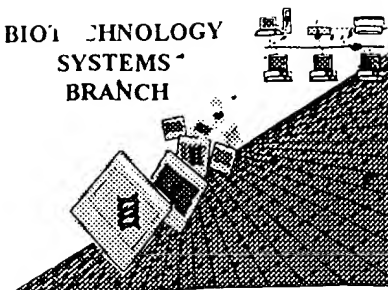
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____ 09/931007 _____

Source: _____ OIPE _____

Date Processed by STIC: _____ 08/27/2001 _____

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/931007_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
     Wrapped Aminos ·   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
                       prevent "wrapping."

2____Invalid Line Length   The rules require that a line not **exceed 72 characters** in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
     Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
                   ensure your subsequent submission is saved in ASCII text.**

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
                       each n or Xaa can only represent a single residue.** Please present the maximum number of each
                       residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
     "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                   previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                   the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
                   Artificial or Unknown sequences.**

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
     (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                       (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                       (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                       This sequence is intentionally skipped

                       Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for each skipped sequence.
     (NEW RULES)   <210> sequence id number
                       <400> sequence id number
                       000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                       In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
      Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
                       is Artificial Sequence

11_✓_Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                     "Unknown." Please explain source of genetic material in <220> to <223> section.
                     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
      "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                   listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING   DATE: 08/27/2001
PATENT APPLICATION: US/09/931,007   TIME: 12:54:35

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\08272001\I931007.raw**

```
 3 <110> APPLICANT: Aventis Pharma S.A.
 5 <120> TITLE OF INVENTION: SYSTEM FOR REGULATING IN VIVO THE EXPRESSION OF A TRANSGENE
BY
 6        CONDITIONAL INHIBITION
 8 <130> FILE REFERENCE: 03806.0512
```
C--> 10 **<140> CURRENT APPLICATION NUMBER: US/09/931,007**
C--> 10 **<141> CURRENT FILING DATE: 2001-08-17**
```
10 <150> PRIOR APPLICATION NUMBER: FR 00/10730
11 <151> PRIOR FILING DATE: 2000-08-18
13 <150> PRIOR APPLICATION NUMBER: US 60/239,246
14 <151> PRIOR FILING DATE: 2000-10-11
16 <160> NUMBER OF SEQ ID NOS: 11
18 <170> SOFTWARE: PatentIn version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 688
22 <212> TYPE: PRT
23 <213> ORGANISM: Homo sapiens,
25 <220> FEATURE:
```
W--> 26 **<221> NAME/KEY: misc** *OK*
```
27 <222> LOCATION: (1)..(688)
28 <223> OTHER INFORMATION: Sequence for PPAR-gamma-2-gamma-2, a modified human PPAR-
gamma (P
29        eroxisome Proliferator Activated Receptor-gamma)
32 <400> SEQUENCE: 1
34 Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
35 1               5                   10                  15
37 Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
38              20                  25                  30
40 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
41          35                  40                  45
43 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
44      50                  55                  60
46 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
47 65                  70                  75                  80
49 Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp
50                  85                  90                  95
52 Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
53              100                 105                 110
55 Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Arg Asn Lys Cys
56          115                 120                 125
58 Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn
59      130                 135                 140
61 Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu
62 145                 150                 155                 160
64 Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp
65                  165                 170                 175
67 Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe
68              180                 185                 190
```

Does Not Comply
Corrected Diskette Needed
See page 4 of 7

70 Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr

RAW SEQUENCE LISTING   DATE: 08/27/2001
PATENT APPLICATION: US/09/931,007   TIME: 12:54:35

Input Set : A:\ES.txt
Output Set: N:\CRF3\08272001\I931007.raw

```
71            195                200                205
73 Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly
74        210                215                220
76 Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser
77 225                230                235                240
79 Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val
80                245                250                255
82 Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe
83                260                265                270
85 Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val
86        275                280                285
88 His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly
89        290                295                300
91 Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys
92 305                310                315                320
94 Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe
95                325                330                335
97 Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile
98     .  340                345                350
100 Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn
101        355                360                365
103 Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu
104    370                375                380
106 Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys
107 385                ·390                395                400
109 Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val
110                405                410                415
112 Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His
113        420                425                430
115 Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr Ala Trp Ala Ile Leu
116        435                440                445
118 Thr Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn
119    450                455                460
121 Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro
122 465                470                475                480
124 Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys
125                485                490                495
127 Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys
128        500                505                510
130 Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu
131        515                520                525
133 Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu
134    530                535                540
136 Met Asn Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr
137 545                550                555                560
139 Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu
140                565                570                575
142 Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp
143    ·  580                585                590
```

RAW SEQUENCE LISTING   DATE: 08/27/2001
PATENT APPLICATION: US/09/931,007   TIME: 12:54:35

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\08272001\I931007.raw**

```
145 Ser Asp Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg
146         595             600             605
148 Pro Gly Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu
149     610             615             620
151 Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser
152 625             630             635             640
154 Gln Leu Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile
155             645             650             655
157 Val Thr Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr
158         660             665             670
160 Asp Met Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
161         675             680             685
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 19
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
```
W--> ```168 <220> FEATURE:``` ~~Errored~~
W--> ```168 <223> OTHER INFORMATION:```
```
168 <400> SEQUENCE: 2
169 tcaaccttta ccctggtag                                        19
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 13
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
```
W--> ```177 <220> FEATURE:```
W--> ```177 <223> OTHER INFORMATION:```
```
177 <400> SEQUENCE: 3
178 aggtcaaagg tca                                              13
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 30
183 <212> TYPE: DNA
```
C--> ```184 <213> ORGANISM: Artificial primer```
W--> ```186 <220> FEATURE:```
W--> ```186 <223> OTHER INFORMATION:```
```
186 <400> SEQUENCE: 4
187 atgcatcgat ggccgcttcg agcagacatg                            30
190 <210> SEQ ID NO: 5
191 <211> LENGTH: 39
192 <212> TYPE: DNA
```
C--> ```193 <213> ORGANISM: Artificial primer```
W--> ```195 <220> FEATURE:```
W--> ```195 <223> OTHER INFORMATION:```
```
195 <400> SEQUENCE: 5
196 atgcgtcgac tctagccgat tttaccacat ttgtagagg                  39
199 <210> SEQ ID NO: 6
200 <211> LENGTH: 33
201 <212> TYPE: DNA
```
C--> ```202 <213> ORGANISM: Artificial primer```
W--> ```204 <220> FEATURE:```

[Handwritten annotation:] A 213 response of "Artificial Sequence" requires an explanation or description of the genetic source in field 223

[Handwritten annotation:] The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING   DATE: 08/27/2001
PATENT APPLICATION: US/09/931,007   TIME: 12:54:35

Input Set : A:\ES.txt
Output Set: N:\CRF3\08272001\I931007.raw

```
W--> 204 <223> OTHER INFORMATION:
     204 <400> SEQUENCE: 6
     205 cgagcatgct gctgctgctg ctgctgctgg gcc                            33
     208 <210> SEQ ID NO: 7
     209 <211> LENGTH: 33
     210 <212> TYPE: DNA
C--> 211 <213> ORGANISM: Artificial primer
W--> 213 <220> FEATURE:
W--> 213 <223> OTHER INFORMATION:
     213 <400> SEQUENCE: 7
     214 gggtctagat taacccgggt gcgcggcgtc ggt                            33
     217 <210> SEQ ID NO: 8
     218 <211> LENGTH: 20
     219 <212> TYPE: DNA
C--> 220 <213> ORGANISM: Artificial primer
W--> 222 <220> FEATURE:
W--> 222 <223> OTHER INFORMATION:
     222 <400> SEQUENCE: 8
     223 cgatcatgtt cgacgacgcc                                          20
     226 <210> SEQ ID NO: 9
     227 <211> LENGTH: 20
     228 <212> TYPE: DNA
C--> 229 <213> ORGANISM: Artificial primer
W--> 231 <220> FEATURE:
W--> 231 <223> OTHER INFORMATION:
     231 <400> SEQUENCE: 9
     232 ccaggtcgca ggcggtgtag                                          20
     235 <210> SEQ ID NO: 10
     236 <211> LENGTH: 23
     237 <212> TYPE: RNA
     238 <213> ORGANISM: Artificial sequence, aptamer
W--> 240 <220> FEATURE:
W--> 240 <223> OTHER INFORMATION:
     240 <400> SEQUENCE: 10
     241 ggccugggcg agaaguuuag gcc                                      23
     244 <210> SEQ ID NO: 11
     245 <211> LENGTH: 72
     246 <212> TYPE: RNA
     247 <213> ORGANISM: Artificial sequence, aptamer
W--> 249 <220> FEATURE:
W--> 249 <223> OTHER INFORMATION:
     249 <400> SEQUENCE: 11
     250 ggugaucaga uucugaucca auguuaugcu ucucugccug ggaacagcug ccugaagcuu   60
     252 uggauccguc gc                                                  72
```

VERIFICATION SUMMARY   DATE: 08/27/2001
PATENT APPLICATION: **US/09/931,007**   TIME: 12:54:36

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\08272001\I931007.raw**

```
L:10  M:270 C: Current Application Number differs, Replaced Current Application No
L:10  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:26  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:168 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:168 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:177 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:177 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:184 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:186 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:186 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:193 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:195 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:195 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:202 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:204 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:204 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:211 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:213 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:213 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:220 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:222 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:222 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:229 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:231 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:231 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:240 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:240 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:249 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:249 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
```